

L Number	Hits	Search Text	DB	Time stamp
1	4	rhodes-kenneth.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/11/13 13:46
2	2	an-wenqian.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/11/13 13:50
3	3	pcip same 9q	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/11/13 13:50

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UMBILICAL ENDOTHELIAL CELL;
 RA Ohya S., Imaizumi Y.;
 RT "human potassium channel interacting protein 2b.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AB044584; BAA96740.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 270 AA; 30959 MW; 22DBD64A15966D98 CRC64;

Query Match 98.6%; Score 1407; DB 4; Length 270;
 Best Local Similarity 98.5%; Pred. No. 2.2e-108;
 Matches 266; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MRGQGRKESLSDSRDLGSGYDQLTGHPPGPTKKALKQRFLKLLPCCGPQALPSVSETLAA 60
 |||||
 Db 1 MRGQGRKESLSDSRDLGSGYDQLTGHPPGPTKKALKQRFLKLLPCCGPQVLPSVSETLAA 60
 |||||
 Qy 61 PASLRPHRPRLLDPDSVDEFEFELSTVCHRPEGLEQLQEQTKFTRKELQVLYRGFKNECPS 120
 |||||:|||||
 Db 61 PASLRPHRPRLLDPDSVEDEFELSTVCHRPEGLEQLQEQTKFTRKELQVLYRGFKNECPS 120
 |||||:|||||
 Qy 121 GIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTHDGSVSFEDFVAGLSVILRGTVDDR 180
 |||||
 Db 121 GIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTHDGSVSFEDFVAGLSVILRGTVDDR 180
 |||||
 Qy 181 LNWFNLYDLNKGDCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
 |||||
 Db 181 LNWFNLYDLNKGDCITKEEMLDIMKSIYDMMGKYTPALREEPPREHVESFFQKMDRKN 240
 |||||
 Qy 241 DGVVTIEEFIESCQKDNIMRSMQLFDNVI 270
 |||||
 Db 241 DGVVTIEEFIESCQKDNIMRSMQLFDNVI 270
 |||||

RESULT 3

Q9JJ69

ID Q9JJ69 PRELIMINARY; PRT; 270 AA.

AC Q9JJ69;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE POTASSIUM CHANNEL-INTERACTING PROTEIN 2A.

GN KCHIP2A.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA Ohya S., Imaizumi Y.;

RT "mouse potassium channel interacting protein 2a (KChip2a).";

RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: TO EF-HAND FAMILY.

DR EMBL; AB044570; BAA96738.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.

DR PRINTS; PR00450; RECOVERIN.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR SMART; SM00054; EFh; 1.
KW Calcium-binding.
SQ SEQUENCE 270 AA; 30906 MW; 917E564A159679C1 CRC64;

Query Match 98.6%; Score 1407; DB 11; Length 270;
Best Local Similarity 98.5%; Pred. No. 2.2e-108;
Matches 266; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 MRGQGRKESLSDSRDLGSDYDQLTGHPGPTKKALKQRFLKLLPCCGPQALPSVSETLAA 60
    |||
Db 1 MRGQGRKESLSDSRDLGSDYDQLTGHPGPTKKALKQRFLKLLPCCGPQVLPVSVSETLAA 60

Qy 61 PASLRPHRPRLLDPDSVDEFEFELSTVCHRPEGLEQLQEQTkFTRKELQVLYRGFKNECPS 120
    |||
Db 61 PASLRPHRPRLLDPDSVEFEFELSTVCHRPEGLEQLQEQTkFTRKELQVLYRGFKNECPS 120

Qy 121 GIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGVSFEDFVAGLSVILRGTVDDR 180
    |||
Db 121 GIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGVSFEDFVAGLSVILRGTVDDR 180

Qy 181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRDK 240
    |||
Db 181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRSK 240

Qy 241 DGVVTIEEFIESCQKDNIMRSMQLFDNVI 270
    |||
Db 241 DGVVTIEEFIESCQKDNIMRSMQLFDNVI 270
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RESULT 4

Q9JI23

ID Q9JI23 PRELIMINARY; PRT; 270 AA.
AC Q9JI23;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE POTASSIUM CHANNEL AUXILIARY SUBUNIT KCHIP2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Takimoto K.;
RT "Potassium channel auxiliary subunit KCHIP2 splicing variant.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: TO EF-HAND FAMILY.
DR EMBL; AF269283; AAF81755.1; -.
DR InterPro; IPR001125; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; efhand; 3.
DR PRINTS; PR00450; RECOVERIN.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR SMART; SM00054; EFh; 1.
KW Calcium-binding.
SQ SEQUENCE 270 AA; 30932 MW; C797DEC90FDC3B92 CRC64;

Query Match 97.4%; Score 1390; DB 11; Length 270;
Best Local Similarity 96.7%; Pred. No. 5.6e-107;
Matches 261; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 MRGQGRKESLSDSRDLGSDYDQLTGHPGPTKKALKQRFLKLLPCCGPQALPSVSETLAA 60
    |||
Db 1 MRGQGRKESLSESRDLGSDYDQLTGHPGPTKALKQRFLKLLPCCGPQALPSVSETLAA 60

Qy 61 PASLRPHRPRLLDPDSVDEFEFELSTVCHRPEGLEQLQEQTkFTRKELQVLYRGFKNECPS 120
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Db      61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTFRRELQVLYRGFKNECPS 120
QY      121 GIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGVSVSFEDFVAGLSVILRGTVDDR 180
Db      121 GIVNEENFKQIYSQFFPQGDSSNYATFLFNAFDTNHDGVSVSFEDFVAGLSVILRGTTDDR 180
QY      181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
Db      181 LSWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
QY      241 DGVVTIEEFIESCQKQDENIMRSMQLFDNVI 270
Db      241 DGVVTIEEFIESCQQDENIMRSMQLFDNVI 270

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SEQ ID NO: 26

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RESULT 1
US-09-048-889-3
; Sequence 3, Application US/09048889
; Patent No. 6117989
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Patterson, Chandra
;   TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/048,889
;     FILING DATE: Herewith
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Cerrone, Michael C
;     REGISTRATION NUMBER: 39,132
;     REFERENCE/DOCKET NUMBER: PF-0493 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-855-0555
;     TELEFAX: 650-845-4166
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 188 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     IMMEDIATE SOURCE:
;       LIBRARY: BRAINON01

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UIS-09-048-889-3

Matches 149: Conservative 26: Mismatches 13: Indels 0: Gaps 0:

Db 181 MOLFENVI 188

RESULT 1

Q9JM60

SQ SEQUENCE 220 AA; 25576 MW; A7093C9456A2838E CRC64;

Matches 219; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 121 VILRGTVDDRLNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTYPALREEAPREHVE 180

Qy 181 NFFQKMDRNDKGVVTIEEFIESCQKDNIMRSMQLFDNVI 220
 :|||||
 Db 181 SFFQKMDRNDKGVVTIEEFIESCQKDNIMRSMQLFDNVI 220

RESULT 2

Q9HD11

ID Q9HD11 PRELIMINARY; PRT; 220 AA.
 AC Q9HD11;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE CARDIAC VOLTAGE GATED POTASSIUM CHANNEL MODULATORY SUBUNIT, SHORT FORM
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CARDIAC;
 RA Juang G.J., Tomaselli G.F.;
 RT "Modulatory elements of voltage gated potassium channels."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF295076; AAG02120.1; -.
 KW Ionic channel.
 FT NON_TER 220 220
 SQ SEQUENCE 220 AA; 25562 MW; 52FD8C601356338F CRC64;

Query Match 99.3%; Score 1149; DB 4; Length 220;
 Best Local Similarity 99.1%; Pred. No. 6.7e-84;
 Matches 218; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGQGRKESLSDSRDLGSDYQLTDSVEDEFELSTVCHRPEGLEQLQEQTKEFKELQVL 60
 :|||||
 Db 1 MRGQGRKESLSDSRDLGSDYQLTDSVDDEFELSTVCHRPEGLEQLQEQTKEFKELQVL 60
 Qy 61 YRGFKNECPGIVNEENFKQIYSQFFPQGDSSSTYATFLNADFNTNHDGSVSFEDFVAGLS 120
 :|||||
 Db 61 YRGFKNECPGIVNEENFKQIYSQFFPQGDSSSTYATFLNADFNTNHDGSVSFEDFVAGLS 120
 Qy 121 VILRGTVDDRLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
 :|||||
 Db 121 VILRGTVDDRLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
 Qy 181 NFFQKMDRNDKGVVTIEEFIESCQKDNIMRSMQLFDNVI 220
 :|||||
 Db 181 SFFQKMDRNDKGVVTIEEFIESCQKDNIMRSMQLFDNVI 220

RESULT 3

Q9JJ68

ID Q9JJ68 PRELIMINARY; PRT; 220 AA.
 AC Q9JJ68;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE POTASSIUM CHANNEL-INTERACTING PROTEIN 2B.
 GN KCHIP2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Ohya S., Imaizumi Y.;
 RT "mouse potassium channel interacting protein 2b (mKChIP2b).";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AB044571; BAA96739.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 220 AA; 25549 MW; 0907CC9456A28392 CRC64;

Query Match 99.1%; Score 1147; DB 11; Length 220;
 Best Local Similarity 99.1%; Pred. No. 9.7e-84;
 Matches 218; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRGQGRKESLSDSRDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60
      |||
Db      1 MRGQGRKESLSDSRDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60

Qy     61 YRGFKNECPSGIVNEENFKQIYSQFFPQGDSSYATFLFNAPDTNHDGSVSFEDFVAGLS 120
      |||
Db     61 YRGFKNECPSGIVNEENFKQIYSQFFPQGDSSYATFLFNAPDTNHDGSVSFEDFVAGLS 120

Qy    121 VILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
      |||
Db    121 VILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180

Qy    181 NFFQKMDRNDKGVVTIEEFIESCQKDENIMRSMQLFDNVI 220
      :|||
Db    181 SFFQKMDRNDKGVVTIEEFIESCQKDENIMRSMQLFDNVI 220
  
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RESULT 4

Q9NS60

ID Q9NS60 PRELIMINARY; PRT; 220 AA.
 AC Q9NS60;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE POTASSIUM CHANNEL-INTERACTING PROTEIN 2C.
 GN KCHIP2C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UMBILICAL ENDOTHELIAL CELL;
 RA Ohya S., Imaizumi Y.;
 RT "human potassium channel interacting protein 2b.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AB044585; BAA96741.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 220 AA; 25586 MW; 57985A40F4CC3B1F CRC64;

Query Match 98.4%; Score 1138; DB 4; Length 220;
 Best Local Similarity 98.6%; Pred. No. 5e-83;
 Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MRGQGRKESLSDSRDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60
      |||
Db      1 MRGQGRKESLSDSRDLGSDYDQLTVSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60
  
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Qy      61 YRGFKNECPSGIVNEENFKQIYSQFFPQGDSSSTYATFLNFAFDTNHDGVSFEDFVAGLS 120
      |||||||
Db      61 YRGFKNECPSGIVNEENFKQIYSQFFPQGDSSSTYATFLNFAFDTNHDGVSFEDFVAGLS 120

Qy     121 VILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
      |||||||
Db     121 VILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEPPREHVE 180

Qy     181 NFFQKMDRNDKGVVTIEEFIESQKQDENIMRSMQLFDNVI 220
      :|||||
Db     181 SFFQKMDRNDKGVVTIEEFIESQKQDENIMRSMQLFDNVI 220

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RESULT 5

Q9HD10

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ID   Q9HD10      PRELIMINARY;      PRT;    227 AA.
AC   Q9HD10;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   CARDIAC VOLTAGE GATED POTASSIUM CHANNEL MODULATORY SUBUNIT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CARDIAC;
RA   Juang G.J., Wu R.C., Tomaselli G.F.;
RT   "Modulatory elements of voltage gated potassium channels.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF295530; AAG02121.1; -.
KW   Ionic channel.
SQ   SEQUENCE    227 AA;  26263 MW;  7F1D2B8E7F85D8B9 CRC64;

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Query Match      98.1%;  Score 1135.5;  DB 4;  Length 227;
Best Local Similarity  96.0%;  Pred. No. 8.2e-83;
Matches 218;  Conservative  2;  Mismatches  0;  Indels  7;  Gaps  1;

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Qy      1 MRGQGRKESLSDSRDLGSDYQLTDSVEDEFELSTVCHRPEGLEQLQEQTKFTRKELQVL 60
      |||||||
Db      1 MRGQGRKESLSDSRDLGSDYQLTDSVDDEFELSTVCHRPEGLEQLQEQTKFTRKELQVL 60

Qy     61 YRGFKN-----ECPSGIVNEENFKQIYSQFFPQGDSSSTYATFLNFAFDTNHDGVSFE 113
      |||||||
Db     61 YRGFKNPGALSFGQCPSGIVNEENFKQIYSQFFPQGDSSSTYATFLNFAFDTNHDGVSFE 120

Qy    114 DFVAGLSVILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREE 173
      |||||||
Db    121 DFVAGLSVILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREE 180

Qy    174 APREHVENFFQKMDRNDKGVVTIEEFIESQKQDENIMRSMQLFDNVI 220
      |||||||
Db    181 APREHVESFFQKMDRNDKGVVTIEEFIESQKQDENIMRSMQLFDNVI 227

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RESULT 6

Q9JI21

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ID   Q9JI21      PRELIMINARY;      PRT;    220 AA.
AC   Q9JI21;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   POTASSIUM CHANNEL AUXILIARY SUBUNIT KCHIP2C.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]

```

RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Takimoto K.;
 RT "Potassium channel auxiliary subunit KCHIP2 splicing variant.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AF269285; AAF81757.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 220 AA; 25618 MW; 519D144AB55A9BBC CRC64;

Query Match 97.7%; Score 1130; DB 11; Length 220;
 Best Local Similarity 96.8%; Pred. No. 2.2e-82;
 Matches 213; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MRGQGRKESLSDSRDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRKELQVL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MRGQGRKESLSERDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRRELQVL 60

QY     61 YRGFKNECPSGIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGSVSFEDFVAGLS 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     61 YRGFKNECPSGIVNEENFKQIYSQFFPQGDSSNYATFLFNAFDTNHDGSVSFEDFVAGLS 120

QY    121 VILRGTVDDRNLNWFNLYDLNKGDCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    121 VILRGTIDDRNLNWFNLYDLNKGDCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180

QY    181 NFFQKMDRNKDGVVTTIEEFIESCQKQDENIMRSMQLFDNVI 220
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    181 SFFQKMDRNKDGVVTTIEEFIESCQQDENIMRSMQLFDNVI 220

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SEQ ID NO: 18

RESULT 14
 US-08-764-563-3
 ; Sequence 3, Application US/08764563
 ; Patent No. 6093565
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/764,563
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0178 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 177 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 458230
 US-08-764-563-3

Query Match 14.9%; Score 212.5; DB 3; Length 177;
 Best Local Similarity 31.6%; Pred. No. 2.6e-15;
 Matches 56; Conservative 44; Mismatches 60; Indels 17; Gaps 6;

QY 89 RPEGLEQLQEQTKFTRRELQVLYRGFK--NECPSGIVNEENFKQIYSQFFPQGDSSNYAT 146
 Db 9 RPVEEVEEMQGTNFTQKEIKKLYKRFFKLDKDGNGTISKDEFLMI-----PELAVNPLVK 63
 QY 147 FLFNAFDTNHDSVSFEDFVAGLSVI-LRGTIDDRNLNWFNLYDLNKDGCITKEEMLDIM 205
 Db 64 RVISIFDENGDSVNFKEFIAALS VFNAQGDQKRLFAFKVYDIDGDGYISNGELFTVL 123
 QY 206 KSIYDMMGKYTYPALREEAPREHVESFFQKMDRNDGVTIEEFIE--SCQQDENIM 260
 Db 124 KM--MVGN----NLSDVQLQQIVDKTILEADEDGDGKISFEEFAKTLSHQDLENKM 173

RESULT 15

US-08-328-322-17

; Sequence 17, Application US/08328322

; Patent No. 5723436

; GENERAL INFORMATION:

; APPLICANT: Huang, Laiqiang

; APPLICANT: Cyert, Martha S.

; TITLE OF INVENTION: Calcineurin Interacting Protein Compositions

; TITLE OF INVENTION: and Methods

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Avenue, Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/328,322

; FILING DATE: 24-OCT-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: P38,615

; REFERENCE/DOCKET NUMBER: 8600-0151.10

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 174 amino acids

; TYPE: amino acid

; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-328-322-17

Query Match 13.4%; Score 191; DB 1; Length 174;
 Best Local Similarity 29.5%; Pred. No. 5.5e-13;
 Matches 52; Conservative 42; Mismatches 66; Indels 16; Gaps 6;

Qy 93 LEQLQEQTkFTRRELQVLYRGFK--NECPsGIVNEENFKQIYSQFFPQGDSSNYATFLFN 150
 :: || || || || || || : | : || :: | | | : | :
 Db 9 VDGLLEDTNFDRDEIERLRKRFMKLDRDSSGSIDKNEFMSI-----PGVSSNPLAGRIME 63
 Qy 151 AFDTNHdGSVSFEDEFVAGLSVIL-RGTIDDRLNWAFNLYDLNKDGCITKEEMLDIMKSIY 209
 || :: || || || :: || || : || :: || || :: || || || : | : ::
 Db 64 VFDADNSGDVDFQEFITGLSIFSGRGSKDEKLRFAFKIYDIDKDGFIENGELFIVLKI-- 121
 Qy 210 DMMGKYTPALREEAPREHVESFFQKMDRNKdGVVTIEEFIESCQQDENIMRSMQL 265
 || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 122 -MVGS---NLDDEQLQQIVDRtIVENDSDGDGRLSFEFEKNAIETTE-VAKSLTL 171

SEQ ID NO: 16

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1363	100.0	257	21	AAy93469	Amino acid sequenc
2	1360	99.8	270	21	AAy93470	Amino acid sequenc
3	1330	97.6	270	21	AAy93468	Amino acid sequenc
4	1242	91.1	252	21	AAy93472	Amino acid sequenc
5	1219	89.4	252	21	AAy93471	Amino acid sequenc
6	1216	89.2	252	21	AAy93475	Amino acid sequenc
7	1216	89.2	252	21	AAy93482	Amino acid sequenc
8	1043	76.5	225	21	AAy93476	Amino acid sequenc
9	1035	75.9	220	21	AAy93473	Amino acid sequenc
10	1035	75.9	220	21	AAy93474	Amino acid sequenc
11	888	65.2	250	21	AAy93495	Amino acid sequenc
12	856	62.8	229	21	AAy93494	Amino acid sequenc

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	464	34.0	190	2	I51686	frequenin - Africa
2	440	32.3	190	2	A55666	neurocalcin - frui
3	434	31.8	193	2	JC2186	hippocalcin - huma
4	428	31.4	191	2	JH0815	neural visinin-lik
5	427	31.3	190	2	S58303	related to neurona
6	426	31.3	193	2	JH0816	neural visinin-lik
7	426	31.3	193	2	I50676	gene Rem-1 protein
8	425	31.2	191	2	JH0605	neural visinin-lik
9	425	31.2	191	2	A48979	visinin-like prote
10	425	31.2	193	2	JH0616	neurocalcin (clone
11	424	31.1	193	2	S47565	calcium-binding pr
12	422.5	31.0	220	2	T33465	hypothetical prote
13	414	30.4	190	2	S61168	hypothetical prote
14	412	30.2	195	2	JC1347	hippocalcin - rat
15	407.5	29.9	254	2	T29566	

Result No.	Score	% Query		DB	ID	Description
		Match	Length			

1	464	34.0	189	1	NCS1_XENLA	Q91614	xenopus lae
2	463	34.0	189	1	NCS1_HUMAN	P36610	homo sapien
3	454	33.3	190	1	APLC_APLCA	Q16981	aplysia cal
4	448	32.9	190	1	NCS1_CAEL	P36608	caenorhabdi
5	441	32.4	192	1	HIPP_RAT	P32076	rattus norv
6	440	32.3	189	1	NCAH_DROME	P42325	drosophila
7	434	31.8	192	1	HIPP_HUMAN	P41211	homo sapien
8	432	31.7	192	1	NECX_APLCA	Q16982	aplysia cal
9	428.5	31.4	186	1	FREQ_DROME	P37236	drosophila
10	428	31.4	190	1	VIS2_RAT	P35332	rattus norv
11	427	31.3	189	1	NCS1_SCHPO	Q09711	schizosacch
12	426	31.3	192	1	VIS3_CHICK	P42324	gallus gall
13	426	31.3	192	1	VIS3_MOUSE	P35333	mus musculu
14	425	31.2	190	1	VIS1_MOUSE		

RESULT 1

ID 0

AC 09JI23:

DT 01-OCT-

DT 01-OCT-2000 (TrEMBLrel. 15, Last seq

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE POTASSIUM CHANNEL AUXILIARY SUBUNIT KCHIP2A.

OS *Rattus norvegicus* (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY;

RA Takimoto K.;

RT "Potassium channel auxiliary subunit KCHIP2 splicing variant.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: TO EF-HAND FAMILY.
 EF EF01 120610000 110610000

DR EMBL; AF269283; AAF81755.1; -.
BB JntouBac JBB001125

DR InterPro; IPR001125; -.
 PP InterPro; IPR002048.

```
DR      InterPro; IPR002048; -.
DR      Pfam; PF00036; afhand; 3
```

DR PRINTS: DB00450: RECOVERY

DB PROSITE: PS00018; EF HAND: UNKNOWN 3

DR SMART: SM00054: FFb: 1

DR SMAR1, SM00054,
KW Calcium-binding

SO SEQUENCE 270 AA: 30932 MW: C797DEC90FDC3B92 CRC64:

Query Match 100.0%; Score 1363; DB 11; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      74 PDSVEDEFELSTVCHRPEGLEQLQEQTKEFTTRRELQVLYRGFKNECPGIVNEENFKQIYS 133
Qy     121 QFFPQGDSSNYATFLFNAFDTNHDGVSFEDFVAGLSVILRGTTIDRLSWAFNLYDLNKD 180
Db     134 QFFPQGDSSNYATFLFNAFDTNHDGVSFEDFVAGLSVILRGTTIDRLSWAFNLYDLNKD 193
Qy     181 GCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRNDGVTIEEFIESC 240
Db     194 GCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRNDGVTIEEFIESC 253
Qy     241 QQDENIMRSMQLFDNVI 257
Db     254 QQDENIMRSMQLFDNVI 270

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SEQ ID NO: 18

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1428	100.0	270	21	AA93470	Amino acid sequenc
2	1395	97.7	270	21	AA93468	Amino acid sequenc
3	1360	95.2	257	21	AA93469	Amino acid sequenc
4	1302	91.2	252	21	AA93472	Amino acid sequenc
5	1284	89.9	252	21	AA93471	Amino acid sequenc
6	1276	89.4	252	21	AA93475	Amino acid sequenc
7	1276	89.4	252	21	AA93482	Amino acid sequenc
8	1100	77.0	220	21	AA93473	Amino acid sequenc
9	1100	77.0	220	21	AA93474	Amino acid sequenc
10	1040	72.8	225	21	AA93476	Amino acid sequenc
11	895.5	62.7	250	21	AA93495	Amino acid sequenc
12	861	60.3	229	21	AA93494	Amino acid sequenc
13	861	60.3	233	21	AA93484	Amino acid sequenc
14	823.5	57.7	216	21	AA93464	Amino acid sequenc
15	823	57.6	188	20	AA42751	Human calcium

RESULT 1

AA93470

ID AA93470 standard; Protein; 270 AA.

XX

AC AA93470;

XX

DT 25-SEP-2000 (first entry)

XX

DE Amino acid sequence of a potassium channel interactor protein.

XX

KW Potassium channel interactor; PCIP; potassium channel; epilepsy;
KW spinocerebellar ataxia; nervous system disorder; cardiovascular disorder;
KW transient outward current.

XX

OS Mus musculus.

XX

PN WO200031133-A2.

XX

PD 02-JUN-2000.

XX

PF 19-NOV-1999; 99WO-US27428.

XX

PR 20-NOV-1998, 98US-0109333.

PR 25-NOV-1998, 98US-0110033.

PR 30-NOV-1998, 98US-0110277.

PR 23-APR-1999, 99US-0298731.

PR 09-JUL-1999, 99US-0350614.

PR 09-JUL-1999, 99US-0350874.

PR 21-SEP-1999, 99US-0399913.

PR 21-SEP-1999; 99US-0400492.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Rhodes K, Betty M, Ling H, An W;
 XX
 DR WPI; 2000-400043/34.
 DR N-PSDB; AAA93470.
 XX
 PT New polynucleotide with homology to the sequence encoding phosphate
 PT channel interacting protein useful in the treatment of e.g. epilepsy
 PT and spinocerebellar ataxia -
 XX
 PS Claim 9; Fig 9; 306pp; English.
 XX
 CC The present sequence represents a potassium channel interactor protein
 CC (PCIP). The PCIP polypeptides bind to a potassium channel, modulate
 CC the activity of a potassium channel protein, and/or modulate a potassium
 CC channel mediated activity in a cell. The polynucleotides and
 CC polypeptides are useful in the treatment of epilepsy, and
 CC spinocerebellar ataxia, as well as nervous system related disorders and
 CC cardiovascular disorders associated with abnormal transient outward
 CC currents. They are also useful for identifying compounds which can
 CC bind to and modulate the expression and function of the PCIP nucleic
 CC acid molecules, and proteins.
 XX
 SQ Sequence 270 AA;

Query Match 100.0%; Score 1428; DB 21; Length 270;
 Best Local Similarity 100.0%; Pred. No. 2e-134;

Issued:

Result No.	Score	Query Match	Length	DB	ID	Description
1	823	57.6	188	3	US-09-048-889-3	Sequence 3, Appli
2	433	30.3	191	3	US-08-655-352-7	Sequence 7, Appli
3	430	30.1	191	3	US-08-655-352-5	Sequence 5, Appli
4	430	30.1	191	3	US-08-655-352-6	Sequence 6, Appli
5	430	30.1	193	3	US-08-655-352-2	Sequence 2, Appli
6	418	29.3	186	3	US-08-655-352-8	Sequence 8, Appli
7	416	29.1	193	3	US-08-655-352-3	Sequence 3, Appli
8	415	29.1	193	3	US-08-655-352-4	Sequence 4, Appli
9	333	23.3	202	1	US-07-804-894-1	Sequence 1, Appli
10	333	23.3	202	1	US-08-419-102-1	Sequence 1, Appli
11	326	22.8	201	1	US-08-820-051-5	Sequence 5, Appli
12	322	22.5	200	1	US-08-820-051-4	Sequence 4, Appli
13	314	22.0	200	1	US-08-820-051-1	Sequence 1, Appli

RESULT 1
 US-09-048-889-3
 ; Sequence 3, Application US/09048889
 ; Patent No. 6117989
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Patterson, Chandra
 ; TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:

7	426	29.8	190	2	S58303	related to neurona
8	426	29.8	193	2	JH0816	neural visinin-lik
9	426	29.8	193	2	I50676	gene Rem-1 protein
10	425	29.8	193	2	JH0616	neurocalcin (clone

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	465	32.6	189	1	NCS1_XENLA Q91614 xenopus lae
2	464	32.5	189	1	NCS1_HUMAN P36610 homo sapien
3	454	31.8	190	1	APLC_APLCA Q16981 aplysia cal
4	450	31.5	190	1	NCS1_CAEEL P36608 caenorhabdi
5	440	30.8	189	1	NCAH_DROME P42325 drosophila
6	440	30.8	192	1	HIPP_RAT P32076 rattus norv
7	433	30.3	190	1	VIS2_RAT P35332 rattus norv
8	433	30.3	192	1	HIPP_HUMAN P41211 homo sapien
9	433	30.3	192	1	NECX_APLCA Q16982 aplysia cal
10	430	30.1	190	1	VIS1_MOUSE P28677 mus musculu
11	428.5	30.0	186	1	FREQ_DROME P37236 drosophila
12	426	29.8	189	1	NCS1_SCHPO Q09711 schizosacch
13	426	29.8	192	1	VIS3_CHICK P42324 gallus gall
14	426	29.8	192	1	VIS3_MOUSE P35333 mus musculu
15	425	29.8	192	1	NECD_BOVIN P29554 bos taurus
16	424	29.7	192	1	VIS3_HUMAN P37235 homo sapien

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1423	99.6	270	11	Q9JI23 Q9ji23 rattus norv
2	1404	98.3	270	11	Q9JM59 Q9jm59 rattus norv
3	1399	98.0	270	4	Q9NS61 Q9ns61 homo sapien
4	1399	98.0	270	11	Q9JJ69 Q9jj69 mus musculu
5	1302	91.2	252	11	Q9JI22 Q9ji22 rattus norv
6	1284	89.9	252	4	Q9NZI1 Q9nzi1 homo sapien
7	1115	78.1	220	11	Q9JI21 Q9ji21 rattus norv
8	1103	77.2	220	11	Q9JM60 Q9jm60 rattus norv
9	1100	77.0	220	4	Q9HD11 Q9hd11 homo sapien
10	1098	76.9	220	11	Q9JJ68 Q9jj68 mus musculu
11	1089	76.3	220	4	Q9NS60 Q9ns60 homo sapien
12	1086.5	76.1	227	4	Q9HD10 Q9hd10 homo sapien
13	1015	71.1	225	4	Q9H0N4 Q9h0n4 homo sapien
14	893.5	62.6	250	11	Q9EQ01 Q9eq01 mus musculu
15	889.5	62.3	250	4	Q9H294 Q9h294 homo sapien
16	861	60.3	216	4	Q9H2A4 Q9h2a4 homo sapien
17	825	57.8	256	11	Q9JHZ5 Q9jhz5 mus musculu

ALIGNMENTS

RESULT 1
Q9JI23
ID Q9JI23 PRELIMINARY; PRT; 270 AA.
AC Q9JI23;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE POTASSIUM CHANNEL AUXILIARY SUBUNIT KCHIP2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY;
 RA Takimoto K.;
 RT "Potassium channel auxiliary subunit KCHIP2 splicing variant.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 CC -|- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AF269283; AAF81755.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 270 AA; 30932 MW; C797DEC90FDC3B92 CRC64;

Query Match 99.6%; Score 1423; DB 11; Length 270;
 Best Local Similarity 99.6%; Pred. No. 2.9e-110;
 Matches 269; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRGQGRKESLSESRLDGSYDQLTGHPGPGSKKALKQRFLLPCCGPQALPSVSETLAA 60
      |||
Db      1 MRGQGRKESLSESRLDGSYDQLTGHPGPGSKKALKQRFLLPCCGPQALPSVSETLAA 60

Qy     61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKFTRRELQVLYRGFKNECPS 120
      |||
Db     61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKFTRRELQVLYRGFKNECPS 120

Qy    121 GIVNEENFKQIYSQFFPQGDSSNYATFLFNAFDTNHDSVSVFEDFVAGLSVILRGITDDR 180
      |||
Db    121 GIVNEENFKQIYSQFFPQGDSSNYATFLFNAFDTNHDSVSVFEDFVAGLSVILRGITDDR 180

Qy    181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
      |||
Db    181 LSWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240

Qy    241 DGVVTIEEFIESCQDENIMRSMQLFDNVI 270
      |||
Db    241 DGVVTIEEFIESCQDENIMRSMQLFDNVI 270

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RESULT 2
 Q9JM59
 ID Q9JM59 PRELIMINARY; PRT; 270 AA.
 AC Q9JM59;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE A-TYPE POTASSIUM CHANNEL MODULATORY PROTEIN 2B.
 GN RKCHIP2B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Ohya S., Imaizumi Y.;
 RT "A-type potassium channel modulatory protein 2b.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 CC -|- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AB040032; BAA92744.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding; Ionic channel.
 SQ SEQUENCE 270 AA; 30933 MW; 3F70A64A159679DD CRC64;

Query Match 98.3%; Score 1404; DB 11; Length 270;
 Best Local Similarity 97.4%; Pred. No. 1.1e-108;
 Matches 263; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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QY      1 MRGQGRKESLSESRDLGSDYDLTGHPGPGSKKALKQRFLLPCCGPQALPSVSETLAA 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MRGQGRKESLSDSRDLGSDYDLTGHPGPGTKKALKQRFLLPCCGPQVLPSVSETLAA 60

QY     61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRRELQVLYRGFKNECPS 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRKELQVLYRGFKNECPS 120

QY    121 GIVNEENFKQIYSQFFPQGDSSNYATFLFNAFDTNHDGVSFEDFVAGLSVILRGTTDDR 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    121 GIVNEENFKQIYSQFFPQGDSSSTYATFLFNAFDTNHDGVSFEDFVAGLSVILRGTVDDR 180

QY    181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240

QY    241 DGVVTIEEFIESCQDENIMRSMQLFDNVI 270
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    241 DGVVTIEEFIESCQDENIMRSMQLFDNVI 270
  
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SEQ ID NO: 20

Issued:

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1333	100.0	252	4	US-09-399-913-20	Sequence 20, Appl
2	1333	100.0	252	4	US-09-298-731-20	Sequence 20, Appl
3	1309	98.2	270	4	US-09-399-913-14	Sequence 14, Appl
4	1309	98.2	270	4	US-09-298-731-14	Sequence 14, Appl
5	1303	97.7	252	4	US-09-399-913-22	Sequence 22, Appl
6	1303	97.7	252	4	US-09-298-731-22	Sequence 22, Appl
7	1284	96.3	270	4	US-09-399-913-18	Sequence 18, Appl
8	1284	96.3	270	4	US-09-298-731-18	Sequence 18, Appl
9	1277	95.8	252	4	US-09-399-913-28	Sequence 28, Appl
10	1277	95.8	252	4	US-09-399-913-42	Sequence 42, Appl
11	1277	95.8	252	4	US-09-298-731-28	Sequence 28, Appl
12	1219	91.4	257	4	US-09-399-913-16	Sequence 16, Appl
13	1219	91.4	257	4	US-09-298-731-16	Sequence 16, Appl
14	1125	84.4	220	4	US-09-399-913-24	Sequence 24, Appl

RESULT 1

US-09-399-913-20

; Sequence 20, Application US/09399913

; Patent No. 6361971

; GENERAL INFORMATION:

; APPLICANT: Rhodes, Kenneth

; APPLICANT: Betty, Maria

; APPLICANT: Ling, Huai-Ping

; APPLICANT: An, Wenqian

; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR

; FILE REFERENCE: MNI-070CP2

; CURRENT APPLICATION NUMBER: US/09/399,913

; CURRENT FILING DATE: 1999-09-21

; EARLIER APPLICATION NUMBER: USSN 60/110,277

; EARLIER FILING DATE: 1998-11-30

; EARLIER APPLICATION NUMBER: USSN 60/110,033

; EARLIER FILING DATE: 1998-11-25

; EARLIER APPLICATION NUMBER: USSN 60/109,333
 ; EARLIER FILING DATE: 1998-11-20
 ; EARLIER APPLICATION NUMBER: USSN 09/298,731
 ; EARLIER FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: USSN 09/350,614
 ; EARLIER FILING DATE: 1999-07-09
 ; EARLIER APPLICATION NUMBER: USSN 09/350,874
 ; EARLIER FILING DATE: 1999-07-09
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 252
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-399-913-20

Query Match 100.0%; Score 1333; DB 4; Length 252;
 Best Local Similarity 100.0%; Pred. No. 3.6e-138;
 Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SUMMARIES

Result No.	% Query				DB ID	Description
	Score	Match	Length			
1	1333	100.0	252	21	AA93471	Amino acid sequenc
2	1333	100.0	252	23	ABG60592	Human potassium ch
3	1309	98.2	270	21	AA93468	Amino acid sequenc
4	1309	98.2	270	23	ABG60589	Human potassium ch
5	1303	97.7	252	21	AA93472	Amino acid sequenc
6	1303	97.7	252	23	ABG60593	Rat potassium chan
7	1284	96.3	270	21	AA93470	Amino acid sequenc
8	1284	96.3	270	23	ABG60591	Mouse potassium ch
9	1279	95.9	270	23	ABG60617	Rat potassium chan
10	1277	95.8	252	21	AA93475	Amino acid sequenc
11	1277	95.8	252	21	AA93482	Amino acid sequenc
12	1277	95.8	252	23	ABG60596	Rat potassium chan
13	1219	91.4	257	21	AA93469	Amino acid sequenc
14	1219	91.4	257	23	ABG60590	Rat potassium chan
15	1191.5	89.4	277	22	AAM78673	Human protein SEQ
16	1125	84.4	220	21	AA93473	Amino acid sequenc

SUMMARIES

Result No.	% Query				DB ID	Description
	Score	Match	Length			
1	1301	97.6	270	2	JC7631	K+ channel-interac
2	466	35.0	190	2	I51686	frequenin - Africa
3	438	32.9	190	2	A55666	neurocalcin - frui
4	431	32.3	190	2	S58303	related to neurona
5	431	32.3	191	2	JH0815	neural visinin-lik
6	431	32.3	193	2	JC2186	hippocalcin - huma
7	427	32.0	191	2	JH0605	neural visinin-lik
8	427	32.0	191	2	A48979	visinin-like prote
9	423.5	31.8	220	2	T33465	hypothetical prote
10	423	31.7	193	2	JH0816	neural visinin-lik
11	423	31.7	193	2	I50676	gene Rem-1 protein
12	422	31.7	193	2	JH0616	neurocalcin (clone
13	421	31.6	193	2	S47565	calcium-binding pr
14	409.5	30.7	254	2	T29566	hypothetical prote
15	409	30.7	195	2	JC1347	hippocalcin - rat
16	405	30.4	190	2	S61168	hypothetical prote
17	389	29.2	165	2	A44103	neurocalcin beta -
18	353	26.5	190	2	T20725	hypothetical prote

5	1304	97.8	270	6	Q8WN03	Q8wn03 mustela put
6	1303	97.7	252	11	Q9JI22	Q9ji22 rattus norv
7	1301.5	97.6	285	4	Q96T44	Q96t44 homo sapien
8	1301	97.6	270	11	Q9JM59	Q9jm59 rattus norv
9	1296	97.2	270	4	Q9NS61	Q9ns61 homo sapien
10	1296	97.2	270	11	Q9JJ69	Q9jj69 mus musculu
11	1284	96.3	270	11	Q8VHN6	Q8vhn6 mus musculu
12	1279	95.9	270	11	Q9JI23	Q9ji23 rattus norv
13	1125	84.4	220	4	Q9HD11	Q9hdl1 homo sapien
14	1121	84.1	220	11	Q9JM60	Q9jm60 rattus norv

SEQ ID NO: 22

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1329	100.0	252	21	AAV93472	Amino acid sequenc
2	1329	100.0	252	23	ABG60593	Rat potassium chan
3	1305	98.2	270	23	ABG60617	Rat potassium chan
4	1303	98.0	252	21	AAV93471	Amino acid sequenc
5	1303	98.0	252	21	AAV93475	Amino acid sequenc
6	1303	98.0	252	21	AAV93482	Amino acid sequenc
7	1303	98.0	252	23	ABG60592	Human potassium ch
8	1303	98.0	252	23	ABG60596	Rat potassium chan
9	1302	98.0	270	21	AAV93470	Amino acid sequenc
10	1302	98.0	270	23	ABG60591	Mouse potassium ch
11	1279	96.2	270	21	AAV93468	Amino acid sequenc
12	1279	96.2	270	23	ABG60589	Human potassium ch
13	1242	93.5	257	21	AAV93469	Amino acid sequenc
14	1242	93.5	257	23	ABG60590	Rat potassium chan
15	1165.5	87.7	277	22	AAM78673	Human protein SEQ

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1278	96.2	270	2	JC7631	K+ channel-interac
2	464	34.9	190	2	I51686	frequenin - Africa
3	440	33.1	190	2	A55666	neurocalcin - frui
4	434	32.7	193	2	JC2186	hippocalcin - huma
5	428	32.2	191	2	JH0815	neural visinin-lik
6	427	32.1	190	2	S58303	related to neurona
7	426	32.1	193	2	JH0816	neural visinin-lik
8	426	32.1	193	2	I50676	gene Rem-1 protein
9	425	32.0	191	2	JH0605	neural visinin-lik
10	425	32.0	191	2	A48979	visinin-like prote
11	425	32.0	193	2	JH0616	neurocalcin (clone
12	424	31.9	193	2	S47565	calcium-binding pr
13	422.5	31.8	220	2	T33465	hypothetical prote
14	414	31.2	190	2	S61168	hypothetical prote

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	816	61.4	256	1	CSEN_MOUSE	Q9qxt8 mus musculu
2	813	61.2	256	1	CSEN_RAT	Q9jm47 rattus norv
3	809	60.9	256	1	CSEN_HUMAN	Q9y2w7 homo sapien
4	464	34.9	189	1	NCS1_XENLA	Q91614 xenopus lae
5	463	34.8	189	1	NCS1_HUMAN	P36610 homo sapien
6	454	34.2	190	1	APLC_APLCA	Q16981 aplysia cal
7	448	33.7	190	1	NCS1_CAEL	P36608 caenorhabdi
8	441	33.2	192	1	HIPP_HUMAN	P32076 homo sapien

9	440	33.1	189	1	NCAH_DROME	P42325 drosophila
10	432	32.5	192	1	NECX_APLCA	Q16982 aplysia cal
11	428.5	32.2	186	1	FREQ_DROME	P37236 drosophila
12	428	32.2	190	1	VIS2_RAT	P35332 rattus norv
13	427	32.1	189	1	NCS1_SCHPO	Q09711 schizosacch
14	426	32.1	192	1	NCAD_CHICK	O12953 gallus

RESULT 1

CSEN_MOUSE

ID CSEN_MOUSE STANDARD; PRT; 256 AA.

AC Q9QXT8; Q9JHZ5;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calsenilin (DRE-antagonist modulator). (DREAM) (Kv channel-interacting protein 3) (A-type potassium channel modulatory protein 3) (KChIP3).

GN CSEN OR DREAM.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Jo D.G., Kim M., Jung Y.K.;

RT "Cloning and characterization of mouse calsenilin/DREAM.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/NJ; TISSUE=Brain;

RA Deng L., Reid R.E., Leavitt B., Hayden M.;

RT "Allele of Mus musculus Dream/calsenilin gene.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RA Lee H.G., Choi J.K., Choi E.K., Wasco W., Buxbaum J.D., Beier D.R., Kim Y.S.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: CALCIUM-DEPENDENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE DRE ELEMENT OF GENES INCLUDING PDYN AND FOS. MAY PLAY A ROLE IN THE REGULATION OF PSEN2 PROTEOLYTIC PROCESSING. MODULATES K4 VOLTAGE-GATED POTASSIUM CHANNELS (BY SIMILARITY).

CC -!- SUBUNIT: BINDS TO DNA AS A HOMOMULTIMER. ASSOCIATES WITH C-TERMINUS OF PSEN1 AND PSEN2. ASSOCIATES WITH KCN1 (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. ALSO MEMBRANE-BOUND. NUCLEAR (BY SIMILARITY).

CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

CC -----

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CC -----

DR EMBL; AF184624; AAF14576.1; -.

DR EMBL; AF274050; AAF74784.1; -.

DR EMBL; AF300870; AAG17450.1; -.

DR HSSP; P36610; 1G8I.

DR MGD; MGI:1929258; Csen.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; efhand; 3.

DR PRINTS; PR00450; RECOVERIN.

DR ProDom; PD000012; EF-hand; 1.

DR SMART; SM00054, EFh; 3.

DR PROSITE; PS00018; EF_HAND; 2.

KW Transcription regulation; Repressor; Calcium-binding; Repeat;

Query Match 61.4%; Score 816; DB 1; Length 256;
Best Local Similarity 61.8%; Pred. No. 2e-56;
Matches 162; Conservative 41; Mismatches 39; Indels 20; Gaps 7;

Qy	4	QGRKESLSERSLDGSYDQLTGHP---PGPSKKALK---QRFLK---LLPCC-----GPQA	50
		: : : : : : :	
Db	2	QRTKEAVKAS---DGN---LLGDPGRIPLSKRESIKWRPRFTRQALMRCCLIKWLSSA	55
Qy	51	LPSVSESNVEDEFELSTVCHRPEGLEQLQEQTFTRRELQVLYRGFKNECPSGIVNEENF	110
		: : : : : : : :	
Db	56	APQGSDDS-DSELESLTVRHQPEGLDQLQAQTFTKKELQSLYRGFKNECPTGLVEDDTF	114
Qy	111	KQISYQFFPQGDSSNYATFLFNAFDTNHGDSVSFEDFVAGLSVILRGITIDRLSWAFNLY	170
		: : : : : : : : : : : : : : : :	
Db	115	KLIYSQFFPQGDATTYAHFLFNAFDADGNGAIHFEDFVVGLSILLRGTVHEKLKWFNLY	174
Qy	171	DLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRNDQGVVTIEE	230
		: : : : : : : : : : : : : : :	
Db	175	DINKDGCITKEEMLAIMKSIYDMMGRHTYPILEDAPLEHVVERFFQKMDRNDQGVVTIDE	234
Qy	231	FIESCQQDENIMRSMQLFDNVI	252
		: : :	
Db	235	FLETCKQDENITNSMQLFENVI	256

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
1	1329	100.0	252	11	Q9JI22	Q9ji22 rattus norv
2	1326	99.8	252	11	Q8VHN5	Q8vhn5 mus musculu
3	1307	98.3	252	6	Q8WN05	Q8wn05 mustela put
4	1305	98.2	270	11	Q9JI23	Q9ji23 rattus norv
5	1303	98.0	252	4	Q9NZ11	Q9nz11 homo sapien
6	1302	98.0	270	11	Q8VHN6	Q8vhn6 mus musculu
7	1283	96.5	270	6	Q8WN03	Q8wn03 mustela put
8	1279	96.2	270	4	Q96T41	Q96t41 homo sapien
9	1278	96.2	270	11	Q9JMS9	Q9jm59 rattus norv
10	1273	95.8	270	4	Q9NS61	Q9ns61 homo sapien
11	1273	95.8	270	11	Q9JJ69	Q9jj69 mus musculu
12	1271.5	95.7	285	4	Q96T44	Q96t44 homo sapien
13	1122	84.4	220	11	Q9JI21	Q9ji21 rattus norv
14	1119	84.2	220	11	Q8VHN4	Q8vhn4 mus musculu
15	1103	83.0	220	6	Q8WN04	Q8wn04 mustela put
16	1102	82.9	220	11	Q9JM60	Q9jm60 rattus norv
17	1099	82.7	220	4	Q9HD11	Q9hd11 homo sapien
18	1097	82.5	220	11	Q9JJ68	Q9jj68 mus musculu
19	1093	82.2	220	4	Q9NS60	Q9ns60 homo sapien

SEQ ID NO: 24

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1156	100.0	220	21	AAAY93473	Amino acid sequenc
2	1149	99.4	220	21	AAAY93474	Amino acid sequenc
3	1149	99.4	220	23	ABG60594	Human potassium ch
4	1149	99.4	220	23	ABG60595	Monkey potassium c

5	1125	97.3	252	21	AA93471	Amino acid sequenc
6	1125	97.3	252	23	ABG60592	Human potassium ch
7	1121	97.0	270	21	AA93468	Amino acid sequenc
8	1121	97.0	270	23	ABG60589	Human potassium ch
9	1100	95.2	270	21	AA93470	Amino acid sequenc
10	1100	95.2	270	23	ABG60591	Mouse potassium ch
11	1099	95.1	252	21	AA93472	Amino acid sequenc
12	1099	95.1	252	23	ABG60593	Rat potassium chan
13	1095	94.7	270	23	ABG60617	Rat potassium chan
14	1073	92.8	252	21	AA93475	Amino acid sequenc
15	1073	92.8	252	21	AA93482	Amino acid sequenc

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1117	96.6	270	2	JC7631	K+ channel-interac
2	466	40.3	190	2	I51686	frequenin - Africa
3	438	37.9	190	2	A55666	neurocalcin - frui
4	431	37.3	190	2	S58303	related to neurona
5	431	37.3	191	2	JH0815	neural visinin-lik
6	431	37.3	193	2	JC2186	hippocalcin - huma
7	427	36.9	191	2	JH0605	neural visinin-lik
8	427	36.9	191	2	A48979	visinin-like prote
9	423.5	36.6	220	2	T33465	hypothetical prote
10	423	36.6	193	2	JH0816	neural visinin-lik
11	423	36.6	193	2	I50676	gene Rem-1 protein
12	422	36.5	193	2	JH0616	neurocalcin (clone
13	421	36.4	193	2	S47565	calcium-binding pr
14	409.5	35.4	254	2	T29566	hypothetical prote
15	409	35.4	195	2	JC1347	hippocalcin - rat
16	405	35.0	190	2	S61168	hypothetical prote

RESULT 1

JC7631

K+ channel-interacting protein 2, longer splice variant - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7631

R;Ohya, S.; Morohashi, Y.; Muraki, K.; Tomita, T.; Watanabe, M.; Iwatsubo, T.; Imaizumi, Y.

Biochem. Biophys. Res. Commun. 282, 96-102, 2001

A;Title: Molecular cloning and expression of the novel splice variants of K+ channel-interacting protein 2.

A;Reference number: JC7631; MUID:21164705; PMID:11263977

A;Contents: Heart

A;Accession: JC7631

A;Molecule type: mRNA

A;Residues: 1-270 <OHY>

A;Cross-references: DDBJ:AB040032

C;Genetics:

A;Gene: KChIP2L

C;Keywords: potassium channel

Query Match 96.6%; Score 1117; DB 2; Length 270;
Best Local Similarity 81.1%; Pred. No. 4e-76;
Matches 219; Conservative 1; Mismatches 0; Indels 50; Gaps 1;

QY 1 MRGQGRKESLSDSRDLGSDYQLT----- 24
|||||
Db 1 MRGQGRKESLSDSRDLGSDYQLTGHPGPTKKALKQRFLKLLPCCGPQVLPSVSETLAA 60

QY 25 -----DSVDFELSTVCHRPEGLEQLQEQTKEFKELQVLYRGFKNECPS 70
|||:|||||
Db 61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKEFKELQVLYRGFKNECPS 120

Qy	39	RPEGLEQLQEQTFRKELQVLYRGFKNECPSGIVNEENFKQIYSQFFPQGDSSTYATFL	98
		: : : : :: : : :: : : : : :	
Db	9	KPEVVVELTRKTYFTEKEVQQWYKGFIKDPCSQLDATGFQKIYKQFFPFPGDPTKFATFV	68
Qy	99	FNAFDTNHGDVSFEDFVAGLSVILRGTVDDRNLNWFANLYDLNKDCITKEEMLDIMKSI	158
		: : :: : : : :	
Db	69	FNVFDEKDGRIEFSEFIQALSVTSRGTLDCLKRWAFKLYDLNDNGYITRNEMLDIVDAI	128
Qy	159	YDMMGKYTPALREEAPREHVESFFQKMDRNKGUVTIEEFIESCKDENIMRSMQLFDN	218
		: : : : : : : : : : :	
Db	129	YQMVGNTVELPEEENTPEKRVDRIFAMMDKNSDGKLTLQEQEGSKADPSIVQALSlydg	188
Qy	219	VI 220	
		::	
Db	189	LV 190	

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	821	71.0	256	1	CSEN_MOUSE	Q9qxt8 mus musculus
2	815	70.5	256	1	CSEN_RAT	Q9j47 rattus norvegicus
3	813	70.3	256	1	CSEN_HUMAN	Q9y2w7 homo sapiens
4	466	40.3	189	1	NCS1_XENLA	Q91614 xenopus laevis
5	465	40.2	189	1	NCS1_HUMAN	P36610 homo sapiens
6	453	39.2	190	1	APLC_APLCA	Q16981 aplysia californica
7	450	38.9	190	1	NCS1_CAEL	P36608 caenorhabditis elegans
8	438	37.9	189	1	NCAH_DROME	P42325 drosophila melanogaster

9	438	37.9	192	1	HIPP_HUMAN	P32076 homo sapien
10	432	37.4	192	1	NECX_APLCA	Q16982 aplysia cal
11	431	37.3	189	1	NCS1_SCHPO	Q09711 schizosacch
12	431	37.3	190	1	VIS2_RAT	P35332 rattus norv
13	429.5	37.2	186	1	FREQ_DROME	P37236 drosophila
14	427	36.9	190	1	VIS1_HUMAN	P28677 homo sapien
15	423	36.6	192	1	NCAD_CHICK	O12953 gallus gall
16	423	36.6	192	1	NCAD_MOUSE	Q91x97 mus musculu
17	423	36.6	192	1	VIS3_CHICK	P42324 gallus gall

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	1156	100.0	220	4	Q9HD11	Q9hd11 homo sapien
	2	1152	99.7	220	11	Q9JM60	Q9jm60 rattus norv
	3	1151	99.6	220	6	Q8WN04	Q8wn04 mustela put
	4	1147	99.2	220	11	Q9JJ68	Q9jj68 mus musculu
	5	1142.5	98.8	227	4	Q9HD10	Q9hd10 homo sapien
	6	1138	98.4	220	4	Q9NS60	Q9ns60 homo sapien
	7	1135	98.2	220	11	Q8VHN4	Q8vhn4 mus musculu
	8	1130	97.8	220	11	Q9JI21	Q9ji21 rattus norv
	9	1125	97.3	252	4	Q9NZI1	Q9nzi1 homo sapien
	10	1121	97.0	270	4	Q96T41	Q96t41 homo sapien
	11	1120	96.9	252	6	Q8WN05	Q8wn05 mustela put
	12	1117	96.6	270	11	Q9JM59	Q9jm59 rattus norv
	13	1116	96.5	270	6	Q8WN03	Q8wn03 mustela put
	14	1113.5	96.3	285	4	Q96T44	Q96t44 homo sapien
	15	1112	96.2	270	4	Q9NS61	Q9ns61 homo sapien

Q9HD11

ID Q9HD11 PRELIMINARY; PRT; 220 AA.

AC Q9HD11;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Cardiac voltage gated potassium channel modulatory subunit, short form

DE (Kv channel interacting protein 2.2) (Kv channel-interacting protein 2

DE isoform 2) (Fragment).

GN KCNIP2 OR KCHIP2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART;

RA Juang G.J., Tomaselli G.F.;

RT "Modulatory elements of voltage gated potassium channels.";

RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21316438; PubMed=11287421;

RA Baehring R., Dannenberg J., Peters H.C., Leicher T., Pongs O.,

RA Isbrandt D.;

RT "Conserved Kv4 N-terminal Domain Critical for Effects of Kv Channel-

RT interacting Protein 2.2 on Channel Expression and Gating.";

RL J. Biol. Chem. 276:23888-23894 (2001).

RN [3]

RP SEQUENCE FROM N.A.

RA Decher N., Uyguner O.Z., Scherer C., Karaman B., Yuksel-Apak M.,

RA Steinmeyer K., Wollnik B.;

RT "KCHIP2 is a functional interaction partner of human KV4.3: Cloning

RT and expression of a new splice variant of hKCHIP2.";

RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF295076; AAG02120.1; -.

DR EMBL; AF347114; AAK70356.1; -.

DR EMBL; AY026328; AAK07674.1; -.
 DR HSSP; P36610; 1G8I.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 3.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_2
 KW Ionic channel.
 FT NON_TER 220 220
 SQ SEQUENCE 220 AA; 25562 MW; 52FD8C601356338F CRC64;

Query Match 100.0%; Score 1156; DB 4; Length 220;
 Best Local Similarity 100.0%; Pred. No. 1e-84;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGQGRKESLSDSRDLGSDYQLTDSVDDEFELSTVCHRPEGLEQLQEQTKFTRKELQVL 60
 |||||
 Db 1 MRGQGRKESLSDSRDLGSDYQLTDSVDDEFELSTVCHRPEGLEQLQEQTKFTRKELQVL 60
 Qy 61 YRGFKNECPSGIVNEENFKQIYSQFFPQGDSSYATFLNFAFDTNHDGVSFEDFVAGLS 120
 |||||
 Db 61 YRGFKNECPSGIVNEENFKQIYSQFFPQGDSSYATFLNFAFDTNHDGVSFEDFVAGLS 120
 Qy 121 VILRGTVDDRLNWFNLYDLNKGDCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
 |||||
 Db 121 VILRGTVDDRLNWFNLYDLNKGDCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
 Qy 181 SFFQKMDRKNKDGVVTTIEEFIESCQKDENIMRSMQLFDNVI 220
 |||||
 Db 181 SFFQKMDRKNKDGVVTTIEEFIESCQKDENIMRSMQLFDNVI 220

SEQ ID NO: 28

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	1328	100.0	252	21 AAY93475	Amino acid sequenc
2	1328	100.0	252	21 AAY93482	Amino acid sequenc
3	1328	100.0	252	23 ABG60596	Rat potassium chan
4	1303	98.1	252	21 AAY93472	Amino acid sequenc
5	1303	98.1	252	23 ABG60593	Rat potassium chan
6	1279	96.3	270	23 ABG60617	Rat potassium chan
7	1277	96.2	252	21 AAY93471	Amino acid sequenc
8	1277	96.2	252	23 ABG60592	Human potassium ch
9	1276	96.1	270	21 AAY93470	Amino acid sequenc
10	1276	96.1	270	23 ABG60591	Mouse potassium ch
11	1253	94.4	270	21 AAY93468	Amino acid sequenc
12	1253	94.4	270	23 ABG60589	Human potassium ch
13	1216	91.6	257	21 AAY93469	Amino acid sequenc
14	1216	91.6	257	23 ABG60590	Rat potassium chan
15	1139.5	85.8	277	22 AAM78673	Human protein SEQ
16	1073	80.8	220	21 AAY93473	Amino acid sequenc
17	1073	80.8	220	21 AAY93474	Amino acid sequenc
18	1073	80.8	220	23 ABG60594	Human potassium ch
19	1073	80.8	220	23 ABG60595	Monkey potassium c
20	1009	76.0	225	21 AAY93476	Amino acid sequenc

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	1252	94.3	270	2 JC7631	K+ channel-interac
2	451	34.0	190	2 I51686	frequenin - Africa

3	446	33.6	190	2	A55666	neurocalcin - frui
4	440	33.1	193	2	JC2186	hippocalcin - huma
5	432	32.5	193	2	JH0816	neural visinin-lik
6	432	32.5	193	2	I50676	gene Rem-1 protein
7	431	32.5	193	2	JH0616	neurocalcin (clone
8	430	32.4	193	2	S47565	calcium-binding pr
9	428	32.2	191	2	JH0815	neural visinin-lik
10	425	32.0	191	2	JH0605	neural visinin-lik
11	425	32.0	191	2	A48979	visinin-like prote
12	422.5	31.8	220	2	T33465	hypothetical prote
13	418	31.5	195	2	JC1347	hippocalcin - rat
14	414	31.2	190	2	S58303	related to neurona
15	401.5	30.2	254	2	T29566	hypothetical prote
16	400	30.1	190	2	S61168	hypothetical prote
17	386	29.1	165	2	A44103	neurocalcin beta -
18	352.5	26.5	190	2	T20725	hypothetical prote

Result No.	Score	Query Match Length DB	ID	Description
1	794	59.8 256 1	CSEN_MOUSE	Q9qxt8 mus musculu
2	791	59.6 256 1	CSEN_RAT	Q9jm47 rattus norv
3	787	59.3 256 1	CSEN_HUMAN	Q9y2w7 homo sapien
4	451	34.0 189 1	NCS1_XENLA	Q91614 xenopus lae
5	450	33.9 189 1	NCS1_HUMAN	P36610 homo sapien
6	449	33.8 190 1	APLC_APLCA	Q16981 aplysia cal
7	447	33.7 192 1	HIPP_HUMAN	P32076 homo sapien
8	446	33.6 189 1	NCAH_DROME	P42325 drosophila
9	442	33.3 190 1	NCS1_CAEEL	P36608 caenorhabdi
10	438	33.0 192 1	NECX_APLCA	Q16982 aplysia cal
11	432	32.5 192 1	NCAD_CHICK	O12953 gallus gall
12	432	32.5 192 1	NCAD_MOUSE	Q91x97 mus musculu

RESULT 3

CSEN_HUMAN

ID CSEN_HUMAN STANDARD; PRT; 256 AA.

AC Q9Y2W7; Q9UJ84; Q9UJ85;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Calsenilin (DRE-antagonist modulator) (DREAM) (Kv channel-interacting

DE protein 3) (A-type potassium channel modulatory protein 3) (KChIP3).

GN CSEN OR DREAM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98442695; PubMed=9771752;

RA Buxbaum J.D., Choi E.K., Luo Y., Lilliehook C., Crowley A.C.,

RA Merriam D.E., Wasco W.;

RT "Calsenilin: a calcium-binding protein that interacts with the

RT presenilins and regulates the levels of a presenilin fragment.";

RL Nat. Med. 4:1177-1181(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Caudate;

RX MEDLINE=99176420; PubMed=10078534;

RA Carrion A.M., Link W.A., Ledo F., Mellstrom B., Naranjo J.R.;

RT "DREAM is a Ca2+-regulated transcriptional repressor.";

RL Nature 398:80-84(1999).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20140134; PubMed=10676964;

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1303	98.1	252	11	Q9JI22	Q9ji22 rattus norv
2	1300	97.9	252	11	Q8VHN5	Q8vhn5 mus musculu
3	1281	96.5	252	6	Q8WN05	Q8wn05 mustela put
4	1279	96.3	270	11	Q9JI23	Q9ji23 rattus norv
5	1277	96.2	252	4	Q9NZI1	Q9nzi1 homo sapien
6	1276	96.1	270	11	Q8VHN6	Q8vhn6 mus musculu
7	1257	94.7	270	6	Q8WN03	Q8wn03 mustela put
8	1253	94.4	270	4	Q96T41	Q96t41 homo sapien
9	1252	94.3	270	11	Q9JM59	Q9jm59 rattus norv
10	1247	93.9	270	4	Q9NS61	Q9ns61 homo sapien
11	1247	93.9	270	11	Q9JJ69	Q9jj69 mus musculu
12	1245.5	93.8	285	4	Q96T44	Q96t44 homo sapien
13	1096	82.5	220	11	Q9JI21	Q9ji21 rattus norv
14	1093	82.3	220	11	Q8VHN4	Q8vhn4 mus musculu
15	1077	81.1	220	6	Q8WN04	Q8wn04 mustela put
16	1076	81.0	220	11	Q9JM60	Q9jm60 rattus norv
17	1073	80.8	220	4	Q9HD11	Q9hd11